

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 02:49:34 ; Search time 68 seconds

(without alignments)
891.799 Million cell updates/sec

Title: US-09-308-829-2

Perfect score: 1232
Sequence: 1 MKKINIKIVITVILISF.....KDNRIIMKNFSDIYLEK 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1187	96.3	235	16 08NXX2	08NXX2 streptococc
2	1051	85.3	206	2 054512	054512 streptococc
3	556	45.1	232	16 0990N1	0990N1 streptococc
4	393.5	31.9	240	16 08P2R5	08P2R5 streptococc
5	387.5	31.5	234	16 08K807	08K807 streptococc
6	386.5	31.4	234	2 093RR9	093RR9 streptococc
7	386.5	31.4	234	2 08G9K7	08G9K7 streptococc
8	370.5	30.1	210	2 09K2G9	09K2G9 streptococc
9	289	23.5	236	2 09S1H8	09S1H8 streptococc
10	288	23.4	233	16 08N289	08N289 streptococc
11	287.5	23.3	209	2 09LAC6	09LAC6 streptococc
12	287.5	23.3	209	2 09LAE1	09LAE1 streptococc
13	286.5	23.3	209	2 09LAC4	09LAC4 streptococc
14	285.5	23.2	209	2 09R005	09R005 streptococc
15	285.5	23.2	209	2 09LAD0	09LAD0 streptococc
16	285.5	23.2	209	2 09LAD9	09LAD9 streptococc

17	285.5	23.2	209	2 09LAD8	09LAD8 streptococc
18	285	23.1	209	2 09LAD1	09LAD1 streptococc
19	284.5	23.1	209	2 09LAE0	09LAE0 streptococc
20	283.5	23.0	209	2 09LAC5	09LAC5 streptococc
21	283.5	23.0	209	2 09LAD7	09LAD7 streptococc
22	283	23.0	209	2 09LAD2	09LAD2 streptococc
23	282.5	22.9	209	2 09LAC9	09LAC9 streptococc
24	281.5	22.8	209	2 09LAC8	09LAC8 streptococc
25	279.5	22.7	209	2 09LAD5	09LAD5 streptococc
26	279.5	22.7	209	2 09LAD4	09LAD4 streptococc
27	279	22.6	233	16 099XW1	099XW1 streptococc
28	278.5	22.6	209	2 09LAC3	09LAC3 streptococc
29	278.5	22.6	209	2 09LAD6	09LAD6 streptococc
30	273	22.2	256	2 09S1H9	09S1H9 streptococc
31	272.5	22.1	209	2 09LAD3	09LAD3 streptococc
32	271.5	22.0	209	2 09LAC7	09LAC7 streptococc
33	270	21.9	256	2 09X9R8	09X9R8 streptococc
34	226	18.3	240	16 09F0L7	09F0L7 staphylococ
35	226	18.3	240	16 08NXX5	08NXX5 staphylococ
36	219	17.8	241	16 053585	053585 staphylococ
37	219	17.8	256	2 08VLM7	08VLM7 staphylococ
38	216	17.5	242	2 093CC6	093CC6 staphylococ
39	216	17.5	242	16 08NVM3	08NVM3 staphylococ
40	211.5	17.2	237	16 08P0R9	08P0R9 streptococc
41	210	17.0	238	2 08L3E1	08L3E1 streptococc
42	210	17.0	239	2 09EZM7	09EZM7 staphylococ
43	210	17.0	239	16 099T47	099T47 staphylococ
44	210	17.0	251	16 08K6K5	08K6K5 streptococc
45	202.5	16.4	259	16 0938J1	0938J1 streptococc

ALIGNMENTS

RESULT 1

ID	Q8NXX2	PRELIMINARY:	PRT:	235 AA.
AC	Q8NXX2:			
DT	01-OCT-2002 (TREMblrel. 22, Created)			
DT	01-OCT-2002 (TREMblrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMblrel. 23, Last annotation update)			
DE	Exotoxin C.			
GN	SPEC OR SPYMI8.0778.			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
CC	NCBI_taxid=186103;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MGAS8232 / Serotype M18;			
RX	MEDLINE=21927593; PubMed=11917108;			
RA	Smoot J.C., Bairdian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,			
RA	Sylva G.L., Sturdevant D.E., Ricklets S.M., Porcella S.F.,			
RA	Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,			
RA	Kapur V., Daly J.A., Veasy L.G., Musser J.M.;			
RT	"Genome sequence and comparative microarray analysis of serotype M18			
RT	group A Streptococcus strains associated with acute rheumatic fever			
RT	outbreaks";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
RL	EMBL: AEO10008; AL97445.1;			
DR	InterPro: IPR006177; Bctrl_tox.			
DR	InterPro: IPR006123; Staph/Strep_toxin.			
DR	InterPro: IPR006126; Staph/Strep_tox.			
DR	InterPro: IPR006173; Staph_tox_DB.			
DR	Pfam: Pf01123; Staph_stp_toxin; 1.			
DR	Pfam: Pf02876; Staph_stp_toxin; 1.			
DR	PRINTS: PR00279; BACTRLTOXIN.			
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SO	SEQUENCE 235 AA; 27372 MW; 53BD041B958C65B CRC64;			

Query Match 96.3%; Score 1187; DB 16; Length 235;

Best Local Similarity 97.4%; Pred. No. 3 5e-75;
Matches 229; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKKINIKIVITITVILISTYFTYHOSDKDISNVKSDLLAYATTTPYDKCRVNFST 60
DB 1 MKKINIKIVITITVILISTISPIIKSDKDISNVKSDLLAYATTTPDYDCRNFST 60
QY 61 THTLNDPOKYGKDYISSEMSYEAQKFRDHDVDFGLTYILNSHTGEIYGGITPA 120
DB 61 THTLNDPOKYGKDYISSEMSYEAQKFRDHDVDFGLTYILNSHTGEIYGGITPA 120
QY 121 QNNKVNHLGLNLFISGESQNLNNKIIIEKDIYVFOEIDFKIRKLYMDNYKIYATSPY 180
DB 121 QNNKVNHLGLNLFISGESQNLNNKIIIEKDIYVFOEIDFKIRKLYMDNYKIYATSPY 180
QY 181 VSGRIETGKDGKHEQIDLFDSPNECTRSIDIFAKYKDNRIIMKNFSHFDIYLEK 235
DB 181 VSGRIETGKDGKHEQIDLFDSPNECTRSIDIFAKYKDNRIIMKNFSHFDIYLEK 235

RESULT 2

ID 054512 PRELIMINARY: PRT: 206 AA.
AC 054512;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE T1M1 ISOLATE SWE88 SPEC (Exotoxin C) (Fragment).
GN SPEC.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T1M1;
RA MEDLINE-94253335; PubMed-8195383;
RA Norrby-Teglund A., Holm S.E., Norgren M.;
RT "Detection and nucleotide sequence analysis of the spec gene in
RT Swedish clinical group A streptococcal isolates.";
RL J. Clin. Microbiol. 32:705-709(1994).
RN [2]
RP SEQUENCE OF 14-169 FROM N.A.
RC STRAIN-D976;
RA Beesen D.E., Izzo M.W., Fiorentino T.R., Carling R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U02360; AAB59978.2; -
DR EMBL: AF055700; AAD11626.1; -
DR HSSP: P13380; IAN8.
DR InterPro: IPR006177; Bcstr1-tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph.tox.OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox.C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT VARIANT 33 33 N -> D.
FT NON_TER 206 206
SQ SEQUENCE 206 AA; 23955 MW; 14DB9CF06C46C9CB CRC64;

Query Match 85.3%; Score 1051; DB 2; Length 206;
Best Local Similarity 99.0%; Pred. No. 8.6e-66;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 26 QSSSKDISNVKSDLLAYATTTPYDKCRVNFSTHTLNDPOKYGKDYISSEMSYE 85
DB 6 KSDSKDISNVKSDLLAYATTTPYDKCRVNFSTHTLNDPOKYGKDYISSEMSYE 65

QY 86 ASQKFRDHDVDFGLTYILNSHTGEIYGGITPAQNNKVNHLGLNLFISGESQNLNN 145
DB 66 ASQKFRDHDVDFGLTYILNSHTGEIYGGITPAQNNKVNHLGLNLFISGESQNLNN 125
QY 146 KIIIEKDIYVFOEIDFKIRKLYMDNYKIYATSPYSGRIETGKDGKHEQIDLFDSPN 205
DB 126 KIIIEKDIYVFOEIDFKIRKLYMDNYKIYATSPYSGRIETGKDGKHEQIDLFDSPN 185
QY 206 GTRSDIFAKYKDNRIIMKNF 226
DB 186 GTRSDIFAKYKDNRIIMKNF 206

RESULT 3

ID 0990N1 PRELIMINARY: PRT: 232 AA.
AC 0990N1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Putative exotoxin (Superantigen) (Streptococcal pyrogenic exotoxin J)
DE (Exotoxin J precursor).
GN SPEC OR SPY0436.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE-21192684; PubMed-11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian X., Jia H.G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC PubMed-11179302;
RA McCormick J.K., Pragman A.A., Stolpa J.C., Leung D.Y.,
RA Schlievert P.M.;
RT "Functional Characterization of Streptococcal Pyrogenic Exotoxin J, a
RT Novel Superantigen.";
RN Infect. Immun. 69:1381-1388(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE-99093428; PubMed-9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE-21259899; PubMed-11359827;
RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
RT "Immunological and biochemical characterization of streptococcal
RT pyrogenic exotoxins I and J (Spe-I and Spe-J) from Streptococcus
RT pyogenes.";
RL J. Immunol. 166:6711-6719(2001).
DR EMBL: AE006504; AAK33456.1; -
DR EMBL: AF321000; AAG59819.1; -
DR EMBL: AF438523; AAL31570.1; -
DR HSSP: P13380; IAN8.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph.tox.OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox.C; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal: Complete proteome.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 232 AA; 27171 MW; 15D1774768EB2789 CRC64;

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Query Match      45.1%; Score 556; DB 16; Length 232;
Best Local Similarity 48.3%; Pred. No. 2,6e-31;
Matches 113; Conservative 39; Mismatches 76; Indels 6; Gaps 3;

OY 1 MKKINIIKIVFIITVILISTYFTYHOSDSKKDISNVKSDLLVAYTTPYDKDCRVNFTSTHT 60
DB 1 MKRI-----IKTIILVIIIFHFGYSVKSDDS-ENIKDQKQLVAYEIIIPVDTCNIDLT 55
OY 61 THTLINDTPQKRGADYIISSEMSYEASOKFRDHDVDFGLFYILNTHGEYITGGITPA 120
DB 56 THDYIDISSYKKNFNSVSESESYITTKFKNOKVNFGLPYFTFRDYVYIIGGVTPS 115
OY 121 QN-KNVNKKILGNLFISGESQONLNKKIILEKDIYTFQEIDEFKIRKYLMDYKITYDATSP 179
DB 116 VNSNSESKITVGNLIDVOQKTLINPKIDKPIFTIOEFPFKIRQYLMQTKIYDNPSP 175
OY 180 VVSGRIEIGTKDGHQIDLPDSNEGTRSDIFAKYKDNRIINKNKSFHDIYL 233
DB 176 YIKQLEIAINGNKHESFNLYDATSSSTRSDIFKKYKDNKTIINMKFSHPDIYL 229

RESULT 4
O8P2R5 PRELIMINARY; PRT; 240 AA.
AC O8P2R5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Exotoxin G.
GN SPEG OR SPYM18-0201.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Studevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Vasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE009969; AAL9695.1; -.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
KW SEQUENCE 240 AA; 28071 MW; ID90199A92A10900 CRC64;

Query Match      31.9%; Score 393.5; DB 16; Length 240;
Best Local Similarity 37.0%; Pred. No. 5,5e-20;
Matches 87; Conservative 56; Mismatches 85; Indels 7; Gaps 5;

OY 6 IIRIVFIITVILISTYFTY--HOSDSKKDISNVKSDLLVAYTTPYDKDCRVNFTSTHT 63
DB 5 ILRFNIIITIIICSVSYGSQLAYADENLKDRLSRFAVNIITPCDYENVEIAFVTTNS 64
OY 64 LNIIDTQYRGK-DYIISSEMSYEASOKFRDHDVDFGLFYILNTHGEYITGGITPAQN- 122
DB 65 IHIMTKOKRSECLIVYDSIVSLGITDQFIKGDVDFGLPYNFSPPYDNIYGGIVKSN 124
OY 123 --KNVNHKLGNLFISGESQONLNKKIILEKDIYTFQEIDEFKIRKYLMDYKITYDATSPY 180
DB 125 QGNK-SLOPVGILNQDKETIYLPSEAVRIKKKQFTLQEFDFKIRKFLMEKYNIVDSSESY 183

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OY 181 VSGRIEIGTKDGHQIDLPDSPNE-GTRSDIFAKYKDNRIINKNKSFHDIYL 234
DB 184 TSGSLFATKDSKHVEYDLFNKDKLLSRDSFFKRYKDNKIFNSEIISHFDIYLK 238

RESULT 5
O8K807 PRELIMINARY; PRT; 234 AA.
AC O8K807;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Pyrogenic exotoxin G.
GN SPEG OR SPYM3.0155.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; AE014139; AAM78762.1; -.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
KW SEQUENCE 234 AA; 27282 MW; AD112C5F8B06F3D CRC64;

Query Match      31.5%; Score 387.5; DB 16; Length 234;
Best Local Similarity 37.6%; Pred. No. 1,4e-19;
Matches 86; Conservative 54; Mismatches 82; Indels 7; Gaps 5;

OY 12 ITIVILISTYFTY--HOSDSKKDISNVKSDLLVAYTTPYDKDCRVNFTSTHTLINDTQ 69
DB 5 ILTIILISCVFSYGSQALAYADENLKDRLSRFAVNIITPCDYENVEIAFVTTNSIHINTK 64
OY 70 KYRGK-DYIISSEMSYEASOKFRDHDVDFGLFYILNTHGEYITGGITPAQN--KNVN 126
DB 65 OKRSECLIVYDSIVSLGITDQFIKGDVDFGLPYNFSPPYDNIYGGIVKSNQGNK-S 123
OY 127 HKILGNLFISGESQONLNKKIILEKDIYTFQEIDEFKIRKYLMDYKITYDATSPVSGRIE 186
DB 124 LQFVGILNQDKETIYLPSEAVRIKKKQFTLQEFDFKIRKFLMEKYNIVDSSESY 183
OY 187 IGTDKGHQIDLPDSPNE-GTRSDIFAKYKDNRIINKNKSFHDIYL 234
DB 184 LATWDSKHVEYDLFNKDKLLSRDSFFKRYKDNKIFNSEIISHFDIYLK 232

RESULT 6
O93RR9 PRELIMINARY; PRT; 234 AA.
AC O93RR9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Streptococcal group G pyrogenic exotoxin G (SpegG) precursor.
GN SPEGG.
KW Streptococcus equisimilis.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=39086;
RA Seidel P., Gerlach D., Guenther E., Relchardt W., Straube E.,
RT Schmidt K.H.;
RT "Streptococcus dysgalactiae supsp. equisimilis can carry superantigen
RT SPEC like gene.";
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ294849; CAC40152.1; -.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRILTOXIN.
KM Signal.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 234 AA: 27107 MW: 1170CC725B78B098 CRC64;

Query Match 31.4%; Score 386.5; DB 2; Length 234;
Best Local Similarity 35.3%; Pred. No. 1.6e-19;
Matches 83; Conservative 54; Mismatches 91; Indels 7; Gaps 4;

OY 3 KINIKIVFIIITVILISYFTYHOSDSKDISNVKSDLLVATITPYDKRCRVNFSTH 62
DB 2 KITIKITITLSWVLSYGSKLIVY---ADEILKDLKASIRFAYDVPLEYENVEITFVTN 57
OY 63 TLNIDT-OKYRGKDYIISSEMSYEASOKFRKRDHYDVGELFYILNSHTGEYIGGTPAQ 121
DB 58 NIHINTGKKGSCVLYVDISVLSGITDNFIMGKADVGLPNFSSPVDNIYGGVYKHS 117
OY 122 NKNVNH-KLGNLFISGESQONLNKKITILEKDIYFQEIPIKIRKYLMDNKIYDASPY 180
DB 118 DDQQTOSLOFVGLNODGETSLPSYTLIIKHQFTLQEFDFKIRKFLMETYSIYDSERY 177
OY 181 VSGRIEIGTKGKHQHOIDLPSPNNGT-RSDIIPAKYKRNRIINKNFSHPDIYLE 234
DB 178 ISGSFFLATKDSKHVEVDLFNKDKLGLGRNFRFKRYKRNKVFNSSEISHFDIYLK 232

RESULT 7
O8G9K7 PRELIMINARY; PRT: 234 AA.
AC O8G9K7.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Superantigen SPEC.
GN SPEC.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G 39072;
RA MEDLINE=22269278; PubMed=12381468;
RA Sachse S., Seidel P., Gerlach D., Guenther E., Roedel J., Straube E.,
RT Schmidt K.H.;
RT "Superantigen like gene(s) in human pathogenic Streptococcus
RT dysgalactiae, supsp. equisimilis: Genomic localization of the gene
RT encoding streptococcal pyrogenic exotoxin G (SpeG).";
RL FEMS Immunol. Med. Microbiol. 34:159-167 (2002).
DR EMBL; AJ489606; CAD3902.1; -.
DR SEQUENCE 234 AA: 27149 MW: 24A890372B817887 CRC64;

Query Match 31.4%; Score 386.5; DB 2; Length 234;
Best Local Similarity 35.3%; Pred. No. 1.6e-19;
Matches 83; Conservative 54; Mismatches 91; Indels 7; Gaps 4;
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OY 3 KINIKIVFIIITVILISYFTYHOSDSKDISNVKSDLLVATITPYDKRCRVNFSTH 62
DB 2 KITIKITITLSWVLSYGSKLIVY---ADEILKDLKASIRFAYDVPLEYENVEITFVTN 57
OY 63 TLNIDT-OKYRGKDYIISSEMSYEASOKFRKRDHYDVGELFYILNSHTGEYIGGTPAQ 121
DB 58 NIHINTGKKGSCVLYVDISVLSGITDNFIMGKADVGLPNFSSPVDNIYGGVYKHS 117
OY 122 NKNVNH-KLGNLFISGESQONLNKKITILEKDIYFQEIPIKIRKYLMDNKIYDASPY 180
DB 118 DDQQTOSLOFVGLNODGETSLPSYTLIIKHQFTLQEFDFKIRKFLMETYSIYDSERY 177
OY 181 VSGRIEIGTKGKHQHOIDLPSPNNGT-RSDIIPAKYKRNRIINKNFSHPDIYLE 234
DB 178 ISGSFFLATKDSKHVEVDLFNKDKLGLGRNFRFKRYKRNKVFNSSEISHFDIYLK 232

RESULT 8
O9K2G9 PRELIMINARY; PRT: 210 AA.
AC O9K2G9.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Exotoxin G (Fragment).
GN Spe-G.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11227, and 1/5045;
RA Prot T.K., Weller K.D., Martin D., Fraser J.D.;
RT "Multiple alleles of streptococcal pyrogenic exotoxin G gene.";
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233459; AAF60292.1; -.
DR EMBL; AF233454; AAF60291.1; -.
DR HSSP; P13380; 1AN8.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRILTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
FT SEQUENCE 210 AA: 24684 MW: FEEESD36EB079209 CRC64;

Query Match 30.1%; Score 370.5; DB 2; Length 210;
Best Local Similarity 38.9%; Pred. No. 1.9e-18;
Matches 81; Conservative 47; Mismatches 75; Indels 5; Gaps 4;

OY 31 KDISNVKSDLLVATITPYDKRCRVNFSTHTLNIDTQYRGK-DYIISSEMSYEASOK 89
DB 2 ENLMDLKRSLRFAYNIPCDYENVEIAFVTNSHIMTKQKRSCLIVYDVSIGLTDQ 61
OY 90 FKRDHYDVGELFYILNSHTGEYIGGTPAQ-NKNVNH-KLGNLFISGESQONLNKKI 147
DB 62 FKIDKADVGLPNFSSPVDNIYGGIVKHSNOGNK-SLOFVGLNODGETFLPSEV 120
OY 148 ILEKDIYFQEIPIKIRKYLMDNKIYDASPYVSGRIEIGTKGKHQHOIDLPSPNE-G 206
DB 121 RIKKQFTLQEFDFKIRKFLMETKYNIDSESRVTSGLFATKDSKHVEVDLFNKDKL 180
OY 207 TRSDIIPAKYKRNRIINKNFSHPDIYLE 234
DB 181 SRDSFFKRYKRNKVFNSSEISHFDIYLK 208

RESULT 9
O9S1H8
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ID 09S1H8 PRELIMINARY; PRT; 256 AA.
AC 09S1H8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Spex protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12714 type 12;
RX MEDLINE=20374978; PubMed=10913699;
RA Getlach D., Fleischner B., Wagner M., Schmidt K.H., Vettermann S.,
RA Reichardt W.;
RT "Purification and Biochemical Characterization of a Basic Superantigen
RT (SPEX/SME23).";
RL FEWS Microbiol. Lett. 188:153-163(2000).
DR EMBL: AJ245405; CAB51744.1; -
DR HSP: P13163; ISXT; Bcrl_tox.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_tox_C; 1.
DR Pfam: PF02876; Staph_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29706 MW; 873D0BAFBE6DC332 CRC64;

Query Match 23.5%; Score 289; DB 2; Length 256;
Best Local Similarity 32.2%; Pred. No. 1.1e-12;
Matches 78; Conservative 41; Mismatches 105; Indels 18; Gaps 6;

QY 1 MKKINIRKIVFIIIVILISTFYFTHQSDSKDISNVSDLLAYATIPYDKDCRVNFT 60
DB 24 MKKRLIFSFSTFIATISRPVIGLEVDNNSLNIN-----YSTIYEISDVIDPKT 76
DB 77 SH--NLVTKKLDVADARDFINSEMEDEYAANDPFTGKIAVSPFDMNYSKGGKVAYT 134
QY 61 THTLINDTOKY--RGKDYIISSEMSYASQKFRDDHVDVFGI---FYILNSHTGEYI 113
DB 114 YGGLTPAONKVNKHLGNLFISGEQONLNKIIIEKDIYTFPEIDFKIRKYLMDNKI 173
DB 135 YGGITPYOKLOYLKISLVNLMINGKQISVPYNEISTNTKTYTAQEIIDLKVRKFLIAHQ 194
QY 174 YDASPVSYSGRIGETKDGKHE--QIDLPDSNEGTRSDIFAKYKDNRIINKNKNSHPDIY 232
DB 195 YSSGSSYSKSGRLVHTNDNSDKYSFDLF-YGYRDKESIFVYVDNKNKSFNIDKIGHDIE 253
QY 233 LE 234
DB 254 ID 255

RESULT 10
Q9N289 PRELIMINARY; PRT; 233 AA.
AC Q9N289;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Mitogenic exotoxin Z.
GN SMEZ OR SPYM18_2064.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=16103;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbhan K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdavant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL: AE010110; AAL98535.1; -
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_tox_C; 1.
DR Pfam: PF02876; Staph_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 233 AA; 26859 MW; 23E07CC9C06AE866 CRC64;

Query Match 23.4%; Score 288; DB 16; Length 233;
Best Local Similarity 30.6%; Pred. No. 1.2e-12;
Matches 74; Conservative 47; Mismatches 103; Indels 18; Gaps 6;

QY 1 MKKINIRKIVFIIIVILISTFYFTHQSDSKDISNVSDLLAYATIPYDKDCRVNFT 60
DB 1 MKKRLIFSFSTFIATISRPVIGLEVDNNSLNINYSTIN-----YISDVIDPKT 53
DB 61 THTLINDTOKY--RGKDYIISSEMSYASQKFRDDHVDVFGI---FYILNSHTGEYI 113
DB 54 SH--NLVTKKLDVADARDFINSEMEDEYAANDPFTGKIAVSPFDMNYSKGGKVAYT 111
QY 114 YGGLTPAONKVNKHLGNLFISGEQONLNKIIIEKDIYTFPEIDFKIRKYLMDNKI 173
DB 112 YGGITPYOKTSLIPNIPVNLWINGKQISVPYNEISTNTKTYTAQEIIDLKVRKFLIAHQ 171
QY 174 YDASPVSYSGRIGETKDGKHE--QIDLPDSNEGTRSDIFAKYKDNRIINKNKNSHPDIY 232
DB 172 YSSGSSYSKSGRLVHTNDNSDKYSFDLF-YGYRDKESIFVYVDNKNKSFNIDKIGHDIE 230
QY 233 LE 234
DB 231 ID 232

RESULT 11
Q9LAC6 PRELIMINARY; PRT; 209 AA.
AC Q9LAC6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Mitogenic exotoxin Z-20 (Fragment).
GN SMEZ-20.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10989;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143670; AAF66669.1; -
DR HSP: P13163; ISXT;
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_toxin; 1.

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DR Pfam: PF02876; Staph_Strip_tox_C: 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24100 MW; 53049A11599BEA68 CRC64;

Query Match 23.3%; Score 287.5; DB 2; Length 209;
 Best Local Similarity 34.7%; Pred. No. 1,le-12;
 Matches 69; Conservative 35; Mismatches 84; Indels 11; Gaps 5;

QY 44 YTTIPYDKDCRVNSTHTLNIIDTQY--RGKDYIISSEMSYEASOKFRDDHVDVG 100
 ID 09LAC4 PRELIMINARY; PRT; 209 AA.
 AC 09LAC4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DB 13 YSTIYEYSDVIDFKTSH--NLVTKKLDVARDARDFINSMDXYAANDFAGDKIAVFS 70
 QY 101 L----FYILNSHGEYIYGITTPAONKKNVNHKLGNLFISGESQONLNKLTLEKDIYTF 156
 DB 71 VPFDMNVLSSKGVTAATYGGITTPYOKTSPKNI PVNLWINGKQIPVYQISTNKTYYTA 130
 QY 157 QEIDFKIRKYLMDNKKIYDATSPYVSGRIEIGTKDGKHE-QIDLFDSPNEGTRSDIFAKY 215
 DB 131 QEIDLKVRKFLAQHQLYSSSSYKSGRLVFHTNDNSDKYFDTLYTGIRKES-IFKYY 189
 QY 216 KDNRIINMKNSHFDIYLE 234
 DB 190 KDNKSFNIDKIGHLDIEID 208

RESULT 12

Q9LAE1 PRELIMINARY; PRT; 209 AA.
 ID 09LAE1
 AC 09LAE1
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin Z-3 (Fragment).
 GN SMEZ-3.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1681;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143653; AAF66654.1; -.
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph_Strip_toxin.
 DR Pfam: PF01123; Staph_Strip_toxin; 1.
 DR Pfam: PF02876; Staph_Strip_toxin; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24071 MW; PADPCDDLA67271 CRC64;

Query Match 23.3%; Score 287.5; DB 2; Length 209;
 Best Local Similarity 33.7%; Pred. No. 1,le-12;
 Matches 67; Conservative 37; Mismatches 84; Indels 11; Gaps 5;

QY 44 YTTIPYDKDCRVNSTHTLNIIDTQY--RGKDYIISSEMSYEASOKFRDDHVDVG 100
 ID 09R005 PRELIMINARY; PRT; 209 AA.
 AC 09R005
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DB 13 YSTIYEYSDVIDFKTSH--NLVTKKLDVARDARDFINSMDXYAANDFAGDKIAVFS 70
 QY 101 L----FYILNSHGEYIYGITTPAONKKNVNHKLGNLFISGESQONLNKLTLEKDIYTF 156
 DB 71 VPFDMNVLSSKGVTAATYGGITTPYOKTSPKNI PVNLWINGKQISVYNEISTNKTYYTA 130
 QY 157 QEIDFKIRKYLMDNKKIYDATSPYVSGRIEIGTKDGKHE-QIDLFDSPNEGTRSDIFAKY 215
 DB 131 QEIDLKVRKFLAQHQLYSSSSYKSGRLVFHTNDNSDKYSLDLFYGYIRKES-IFKYY 189

QY 216 KDNRIINMKNSHFDIYLE 234
 DB 190 KDNKSFNIDKIGHLDIEID 208

RESULT 13

Q9LAC4 PRELIMINARY; PRT; 209 AA.
 ID 09LAC4
 AC 09LAC4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin Z-22 (Fragment).
 GN SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10463;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143672; AAF66671.1; -.
 DR HSSP: P13163; 1SXT.
 DR InterPro: IPR006123; Staph_Strip_toxin.
 DR InterPro: IPR006173; Staph_Strip_toxin.
 DR Pfam: PF01123; Staph_Strip_toxin; 1.
 DR Pfam: PF02876; Staph_Strip_toxin; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456DEDE8 CRC64;

Query Match 23.3%; Score 286.5; DB 2; Length 209;
 Best Local Similarity 34.2%; Pred. No. 1,3e-12;
 Matches 68; Conservative 37; Mismatches 83; Indels 11; Gaps 5;

QY 44 YTTIPYDKDCRVNSTHTLNIIDTQY--RGKDYIISSEMSYEASOKFRDDHVDVG 100
 ID 09R005 PRELIMINARY; PRT; 209 AA.
 AC 09R005
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DB 13 YSTIYEYSDVIDFKTSH--NLVTKKLDVARDARDFINSMDXYAANDFAGDKIAVFS 70
 QY 101 L----FYILNSHGEYIYGITTPAONKKNVNHKLGNLFISGESQONLNKLTLEKDIYTF 156
 DB 71 VPFDMNVLSSKGVTAATYGGITTPYOKTSPKNI PVNLWINGKQISVYNEISTNKTYYTA 130
 QY 157 QEIDFKIRKYLMDNKKIYDATSPYVSGRIEIGTKDGKHE-QIDLFDSPNEGTRSDIFAKY 215
 DB 131 QEIDLKVRKFLAQHQLYSSSSYKSGRLVFHTNDNSDKYSLDLFYGYIRKES-IFKYY 189
 QY 216 KDNRIINMKNSHFDIYLE 234
 DB 190 KDNKSFNIDKIGHLDIEID 208

RESULT 14

Q9R005 PRELIMINARY; PRT; 209 AA.
 ID 09R005
 AC 09R005
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Mitogenic exotoxin Z 2 (Fragment).
 GN SMEZ-2.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]

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